

SEQUENCE LISTING

<110> Drmanac, Radoje T.
 Labat, Ivan
 Stache-Crain, Birgit
 Dickson, Mark C.
 Jones, Lee William
 Ballinger, Dennis G.
 Xue, Aidong
 Tang, Y. Tom
 Liu, Chenghua
 Asundi, Vinod

<120> STEM CELL MAINTENANCE FACTOR MATERIALS AND METHODS

<130> 28110/35905A

<140> To be assigned

<141> Filed herewith

<150> 09/378,667

<151> 1999-08-20

<150> 09/687,527

<151> 2000-10-12

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 560

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(559)

<220>

<223> hiwi-Hy/CG 389

<400> 1

t tcc att aaa aaa tat ttg agc tya kac tgc cca gtc cca agc caa tgt 49

Ser Ile Lys Lys Tyr Leu Ser Xaa Xaa Cys Pro Val Pro Ser Gln Cys
 1 5 10 15

gtg stt gct cgg acc ttg aat aaa cag ggc atg atg atg agt atc gcc 97

Val Xaa Ala Arg Thr Leu Asn Lys Gln Gly Met Met Met Ser Ile Ala
 20 25 30

acc aag atc gct atg cag atg act tgc aag ctc gga ggc gag ctg tgg 145

Thr Lys Ile Ala Met Gln Met Thr Cys Lys Leu Gly Gly Glu Leu Trp
 35 40 45

gct gtg gaa ata cct tta aag tcc ctg atg gtg gtc ggt att gat gtc 193

Ala Val Glu Ile Pro Leu Lys Ser Leu Met Val Val Gly Ile Asp Val
 50 55 60

tgt aaa gat gca ctc agc aag gac gtg atg gtt gtt gga tgc gtg gcc 241

Cys Lys Asp Ala Leu Ser Lys Asp Val Met Val Val Gly Cys Val Ala
 65 70 75 80

"Sheet 1 of 1"

agt gtt aac ccc aga atc acc agg tgg ttt tcc cgc tgt atc ctt cag 289
Ser Val Asn Pro Arg Ile Thr Arg Trp Phe Ser Arg Cys Ile Leu Gln
85 90 95

aga aca atg act gat gtt gca gat tgc ttg aaa gtt ttc atg act gga 337
Arg Thr Met Thr Asp Val Ala Asp Cys Leu Lys Val Phe Met Thr Gly
100 105 110

gca ctc aac aaa tgg tac aag tac aat cat gat ttg cca gca cgg ata 385
Ala Leu Asn Lys Trp Tyr Lys Tyr Asn His Asp Leu Pro Ala Arg Ile
115 120 125

att gtg tac cgt gct ggt gta ggg gat ggt cag ctg aaa aca ctt att 433
Ile Val Tyr Arg Ala Gly Val Gly Asp Gly Gln Leu Lys Thr Leu Ile
130 135 140

gaa tat gaa gtc cca cag ctg ctg agc agt gtg gca gaa tcc agc tca 481
Glu Tyr Glu Val Pro Gln Leu Leu Ser Ser Val Ala Glu Ser Ser
145 150 155 160

aat acc agc tca aga ctg tcg gtg att gtg gtc agg aag aag tgc atg 529
Asn Thr Ser Ser Arg Leu Ser Val Ile Val Val Arg Lys Lys Cys Met
165 170 175

cca cga ttc ttt acc gaa atg aac cgc act g 560
Pro Arg Phe Phe Thr Glu Met Asn Arg Thr
180 185

<210> 2
<211> 186
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (8)
<223> Xaa = Leu

<220>
<221> SITE
<222> (9)
<223> Xaa = Asp or Tyr

<220>
<221> SITE
<222> (18)
<223> Xaa = Leu or Val

<400> 2
Ser Ile Lys Lys Tyr Leu Ser Xaa Xaa Cys Pro Val Pro Ser Gln Cys
1 5 10 15
Val Xaa Ala Arg Thr Leu Asn Lys Gln Gly Met Met Met Ser Ile Ala
20 25 30
Thr Lys Ile Ala Met Gln Met Thr Cys Lys Leu Gly Gly Glu Leu Trp
35 40 45
Ala Val Glu Ile Pro Leu Lys Ser Leu Met Val Val Gly Ile Asp Val
50 55 60

1002949-1004

Glu Tyr Glu Val Pro Gln Leu Leu Ser Ser Val Ala Glu Ser Ser Ser
145 150 155 160

Asn Thr Ser Ser Arg Leu Ser Val Ile Val Val Arg Lys Lys Cys Met
165 170 175

Pro Arg Phe Phe Thr Glu Met Asn Arg Thr
180 185

<220>
<223> hiwi

<400>	3															
Gly	Val	Ser	Phe	Leu	Glu	Tyr	Tyr	Arg	Lys	Gln	Tyr	Asn	Gln	Glu	Ile	
1				5					10					15		
Thr	Asp	Leu	Lys	Gln	Pro	Val	Leu	Val	Ser	Gln	Pro	Lys	Arg	Arg	Arg	
			20					25					30			
Gly	Pro	Gly	Gly	Thr	Leu	Pro	Gly	Pro	Ala	Met	Leu	Ile	Pro	Glu	Leu	
		35					40					45				
Cys	Tyr	Leu	Thr	Gly	Leu	Thr	Asp	Lys	Met	Arg	Asn	Asp	Phe	Asn	Val	
	50					55					60					
Met	Lys	Asp	Leu	Ala	Val	His	Thr	Arg	Leu	Thr	Pro	Glu	Gln	Arg	Gln	
65					70					75					80	
Arg	Glu	Val	Gly	Arg	Leu	Ile	Asp	Tyr	Ile	His	Lys	Asn	Asp	Asn	Val	
				85					90					95		
Gln	Arg	Glu	Leu	Arg	Asp	Trp	Gly	Leu	Ser	Phe	Asp	Ser	Asn	Leu	Leu	
			100					105					110			
Ser	Phe	Ser	Gly	Arg	Ile	Leu	Gln	Thr	Glu	Lys	Ile	His	Gln	Gly	Gly	
		115					120					125				
Lys	Thr	Phe	Asp	Tyr	Asn	Pro	Gln	Phe	Ala	Asp	Trp	Ser	Lys	Glu	Thr	
	130					135					140					

Arg 145	Gly	Ala	Pro	Leu	Ile	Ser	Val	Lys	Pro	Leu	Asp	Asn	Trp	Leu	Leu
					150					155					160
Ile	Tyr	Thr	Arg	Arg	Asn	Tyr	Glu	Ala	Ala	Asn	Ser	Leu	Ile	Gln	Asn
				165					170					175	
Leu	Phe	Lys	Val	Thr	Pro	Ala	Met	Gly	Met	Gln	Met	Arg	Lys	Ala	Ile
			180					185					190		
Met	Ile	Glu	Val	Asp	Asp	Arg	Thr	Glu	Ala	Tyr	Leu	Arg	Val	Leu	Gln
		195					200					205			
Gln	Lys	Val	Thr	Ala	Asp	Thr	Gln	Ile	Val	Val	Cys	Leu	Leu	Ser	Ser
	210					215					220				
Asn	Arg	Lys	Asp	Lys	Tyr	Asp	Ala	Ile	Lys	Lys	Tyr	Leu	Cys	Thr	Asp
225					230					235					240
Cys	Pro	Thr	Pro	Ser	Gln	Cys	Val	Val	Ala	Arg	Thr	Leu	Gly	Lys	Gln
				245					250					255	
Gln	Thr	Val	Met	Ala	Ile	Ala	Thr	Lys	Ile	Ala	Leu	Gln	Met	Asn	Cys
			260					265					270		
Lys	Met	Gly	Gly	Glu	Leu	Trp	Arg	Val	Asp	Ile	Pro	Leu	Lys	Leu	Val
		275					280					285			
Met	Ile	Val	Gly	Ile	Asp	Cys	Tyr	His	Asp	Met	Thr	Ala	Gly	Arg	Arg
	290					295					300				
Ser	Ile	Ala	Gly	Phe	Val	Ala	Ser	Ile	Asn	Glu	Gly	Met	Thr	Arg	Trp
305					310					315					320
Phe	Ser	Arg	Cys	Ile	Phe	Gln	Asp	Arg	Gly	Gln	Glu	Leu	Val	Asp	Gly
				325					330					335	
Leu	Lys	Val	Cys	Leu	Gln	Ala	Ala	Leu	Arg	Ala	Trp	Asn	Ser	Cys	Asn
			340					345					350		
Glu	Tyr	Met	Pro	Ser	Arg	Ile	Ile	Val	Tyr	Arg	Asp	Gly	Val	Gly	Asp
		355					360					365			
Gly	Gln	Leu	Lys	Thr	Leu	Val	Asn	Tyr	Glu	Val	Pro	Gln	Phe	Leu	Asp
	370					375					380				
Cys	Leu	Lys	Ser	Ile	Gly	Arg	Gly	Tyr	Asn	Pro	Arg	Leu	Thr	Val	Ile
385					390					395					400
Val	Val	Lys	Lys	Arg	Val	Asn	Thr	Arg	Phe	Phe	Ala	Gln	Ser	Gly	Gly
				405					410					415	
Arg	Leu	Gln	Asn	Pro	Leu	Pro	Gly	Thr	Val	Ile	Asp	Val	Glu	Val	Thr
			420					425					430		
Arg	Pro	Glu	Trp	Tyr	Asp	Phe	Phe	Ile	Val	Ser	Gln	Ala	Val	Arg	Ser
		435					440					445			
Gly	Ser	Val	Ser	Pro	Thr	His	Tyr	Asn	Val	Ile	Tyr	Asp	Asn	Ser	Gly
	450					455					460				
Leu	Lys	Pro	Asp	His	Ile	Gln	Arg	Leu	Thr	Tyr	Lys	Leu	Cys	His	Ile
465					470					475					480

Tyr Tyr Asn Trp Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr
485 490 495

Ala His Lys Leu Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro
500 505 510

Asn Leu Ser Leu Ser Asn Arg Leu Tyr Tyr Leu
515 520

<210> 4
<211> 866
<212> PRT
<213> Drosophila

<220>
<223> aubergine

<400> 4
Met Asn Leu Pro Pro Asn Pro Val Ile Ala Arg Gly Arg Gly Arg Gly
1 5 10 15

Arg Lys Pro Asn Asn Val Glu Ala Asn Arg Gly Phe Ala Pro Ser Leu
20 25 30

Gly Gln Lys Ser Asp Pro Ser His Ser Glu Gly Asn Gln Ala Ser Gly
35 40 45

Gly Asn Gly Gly Gly Gly Asp Ala Gln Val Gly Pro Ser Ile Glu Lys
50 55 60

Ser Ser Leu Ser Ala Val Gln Met His Lys Ser Glu Gly Asp Pro Arg
65 70 75 80

Gly Ser Val Arg Gly Arg Arg Leu Ile Thr Asp Leu Val Tyr Ser Arg
85 90 95

Pro Pro Gly Met Thr Ser Lys Lys Gly Val Val Gly Thr His Ile Thr
100 105 110

Val Gln Ala Asn Tyr Phe Lys Val Leu Lys Arg Pro Asn Trp Thr Ile
115 120 125

Tyr Gln Tyr Arg Val Asp Phe Thr Pro Asp Val Glu Ala Thr Arg Leu
130 135 140

Arg Arg Ser Phe Leu Tyr Glu His Lys Gly Ile Leu Gly Gly Tyr Ile
145 150 155 160

Phe Asp Gly Thr Asn Met Phe Cys Ile Asn Gln Phe Lys Ala Val Gln
165 170 175

Asp Ser Pro Tyr Val Leu Glu Leu Val Thr Lys Ser Arg Ala Gly Glu
180 185 190

Asn Ile Glu Ile Lys Ile Lys Ala Val Gly Ser Val Gln Ser Thr Asp
195 200 205

Ala Glu Gln Phe Gln Val Leu Asn Leu Ile Leu Arg Arg Ala Met Glu
210 215 220

Gly Leu Asp Leu Lys Leu Val Ser Arg Tyr Tyr Tyr Asp Pro Gln Ala
225 230 235 240

10029495.10001

Lys	Ile	Asn	Leu	Glu	Asn	Phe	Arg	Met	Gln	Leu	Trp	Pro	Gly	Tyr	Gln	
				245					250							255
Thr	Ser	Ile	Arg	Gln	His	Glu	Asn	Asp	Ile	Leu	Leu	Cys	Ser	Glu	Ile	
				260					265							270
Cys	His	Lys	Val	Met	Arg	Thr	Glu	Thr	Leu	Tyr	Asn	Ile	Leu	Ser	Asp	
				275					280							285
Ala	Ile	Arg	Asp	Ser	Asp	Asp	Tyr	Gln	Ser	Thr	Phe	Lys	Arg	Ala	Val	
				290					295							300
Met	Gly	Met	Val	Ile	Leu	Thr	Asp	Tyr	Asn	Asn	Lys	Thr	Tyr	Arg	Ile	
305					310					315						320
Asp	Asp	Val	Asp	Phe	Gln	Ser	Thr	Pro	Leu	Cys	Lys	Phe	Lys	Thr	Asn	
				325					330							335
Asp	Gly	Glu	Ile	Ser	Tyr	Val	Asp	Tyr	Tyr	Lys	Lys	Arg	Tyr	Asn	Ile	
				340					345							350
Ile	Ile	Arg	Asp	Leu	Lys	Gln	Pro	Leu	Val	Met	Ser	Arg	Pro	Thr	Asp	
				355					360							365
Lys	Asn	Ile	Arg	Gly	Gly	Asn	Asp	Gln	Ala	Ile	Met	Ile	Ile	Pro	Glu	
				370					375							380
Leu	Ala	Arg	Ala	Thr	Gly	Met	Thr	Asp	Ala	Met	Arg	Ala	Asp	Phe	Arg	
385					390					395						400
Thr	Leu	Arg	Ala	Met	Ser	Glu	His	Thr	Arg	Leu	Asn	Pro	Asp	Arg	Arg	
				405					410							415
Ile	Glu	Arg	Leu	Arg	Met	Phe	Asn	Lys	Arg	Leu	Lys	Ser	Cys	Lys	Gln	
				420					425							430
Ser	Val	Glu	Thr	Leu	Lys	Ser	Trp	Asn	Ile	Glu	Leu	Asp	Ser	Ala	Leu	
				435					440							445
Val	Glu	Ile	Pro	Ala	Arg	Val	Leu	Pro	Pro	Glu	Lys	Ile	Leu	Phe	Gly	
				450					455							460
Asn	Gln	Lys	Ile	Phe	Val	Cys	Asp	Ala	Arg	Ala	Asp	Trp	Thr	Asn	Glu	
465					470					475						480
Phe	Arg	Thr	Cys	Ser	Met	Phe	Lys	Asn	Val	His	Ile	Asn	Arg	Trp	Tyr	
				485					490							495
Val	Ile	Thr	Pro	Ser	Arg	Asn	Leu	Arg	Glu	Thr	Gln	Glu	Phe	Val	Gln	
				500					505							510
Met	Cys	Ile	Arg	Thr	Ala	Ser	Ser	Met	Lys	Met	Asn	Ile	Cys	Asn	Pro	
				515					520							525
Ile	Tyr	Glu	Glu	Ile	Pro	Asp	Asp	Arg	Asn	Gly	Thr	Tyr	Ser	Gln	Ala	
				530					535							540
Ile	Asp	Asn	Ala	Ala	Ala	Asn	Asp	Pro	Gln	Ile	Val	Met	Val	Val	Met	
545					550					555						560

Arg Ser Pro Asn Glu Glu Lys Tyr Ser Cys Ile Lys Lys Arg Thr Cys
565 570 575

Val Asp Arg Pro Val Pro Ser Gln Val Val Thr Leu Lys Val Ile Ala
580 585 590

Pro Arg Gln Gln Lys Pro Thr Gly Leu Met Ser Ile Ala Thr Lys Val
595 600 605

Val Ile Gln Met Asn Ala Lys Leu Met Gly Ala Pro Trp Gln Val Val
610 615 620

Ile Pro Leu His Gly Leu Met Thr Val Gly Phe Asp Val Cys His Ser
625 630 635 640

Pro Lys Asn Lys Asn Lys Ser Tyr Gly Ala Phe Val Ala Thr Met Asp
645 650 655

Gln Lys Glu Ser Phe Arg Tyr Phe Ser Thr Val Asn Glu His Ile Lys
660 665 670

Gly Gln Glu Leu Ser Glu Gln Met Ser Val Asn Met Ala Cys Ala Leu
675 680 685

Arg Ser Tyr Gln Glu Gln His Arg Ser Leu Pro Glu Arg Ile Leu Phe
690 695 700

Phe Arg Asp Gly Val Gly Asp Gly Gln Leu Tyr Gln Val Val Asn Ser
705 710 715 720

Glu Val Asn Thr Leu Lys Asp Arg Leu Asp Glu Ile Tyr Lys Ser Ala
725 730 735

Gly Lys Gln Glu Gly Cys Arg Met Thr Phe Ile Ile Val Ser Lys Arg
740 745 750

Ile Asn Ser Arg Tyr Phe Thr Gly His Arg Asn Pro Val Pro Gly Thr
755 760 765

Val Val Asp Asp Val Ile Thr Leu Pro Glu Arg Tyr Asp Phe Phe Leu
770 775 780

Val Ser Gln Ala Val Arg Ile Gly Thr Val Ser Pro Thr Ser Tyr Asn
785 790 795 800

Val Ile Ser Asp Asn Met Gly Leu Asn Ala Asp Lys Leu Gln Met Leu
805 810 815

Ser Tyr Lys Met Thr His Met Tyr Tyr Asn Tyr Ser Gly Thr Ile Arg
820 825 830

Val Pro Ala Val Cys His Tyr Ala His Lys Leu Ala Phe Leu Val Ala
835 840 845

Glu Ser Ile Asn Arg Ala Pro Ser Ala Gly Leu Gln Asn Gln Leu Tyr
850 855 860

Phe Leu
865

<211> 722
<212> PRT
<213> Caenorhabditis elegans

<220>
<223> ciw11

<400> 5

Met	Ile	Gln	Asn	Asp	Tyr	Ser	Ile	Tyr	Gln	Tyr	His	Val	Glu	Phe	Glu	
1				5					10					15		
Pro	Thr	Val	Asp	Ser	Lys	Ala	Thr	Arg	Glu	Asn	Met	Leu	Arg	Gln	Pro	
			20					25					30			
Ser	Val	Thr	Val	Glu	Ile	Gly	Lys	His	Phe	Val	Phe	Asp	Gly	Met	Ile	
		35					40					45				
Leu	Tyr	Leu	Lys	Glu	Glu	Trp	Asp	Gln	Asn	Gln	Met	Ile	Glu	Val	Gln	
	50					55					60					
His	Pro	Asn	Asp	Asn	Ser	Leu	Ile	Cys	Ile	Arg	Phe	Lys	Lys	Thr	Asn	
65					70					75					80	
Arg	Phe	Leu	Val	Asp	Asp	Pro	Gln	Thr	Ile	Asn	Ile	Phe	Asn	Thr	Ile	
				85					90					95		
Ile	Arg	Arg	Ser	Phe	Asp	Ala	Met	Lys	Leu	Thr	Gln	Ile	Gly	Arg	Asn	
			100					105					110			
Tyr	Phe	Asp	Trp	Asp	Asn	Ser	Arg	Ala	Leu	Arg	Lys	Glu	Leu	Arg	Ser	
		115					120					125				
Cys	Gln	Asn	Asn	Arg	Gln	Arg	Val	Gln	Glu	Lys	Met	Asn	Glu	Val	Tyr	
	130					135					140					
Gly	Gly	Ser	Thr	Ile	Ile	Thr	Arg	Tyr	Asn	Asn	Lys	Leu	His	Arg	Phe	
145					150					155					160	
Thr	Arg	Leu	Asp	Asn	Glu	Ile	Thr	Pro	Leu	Ser	Lys	Phe	Gln	Lys	Asp	
			165						170					175		
Gly	Glu	Gln	Ile	Ile	Leu	Lys	Glu	Tyr	Phe	Lys	Asn	Gln	Tyr	Asp	Ile	
			180					185					190			
Asp	Ile	Thr	Asp	Asp	Glu	Gln	Phe	Ile	Ile	Ile	Ser	Glu	Gly	Lys	Pro	
	195						200					205				
Lys	Gln	Pro	Gly	Glu	Pro	Pro	Gln	Val	Asn	Tyr	Ile	Val	Pro	Glu	Leu	
	210					215					220					
Cys	Phe	Pro	Thr	Gly	Leu	Thr	Asp	Glu	Met	Arg	Lys	Asp	Phe	Lys	Met	
225					230					235					240	
Met	Lys	Glu	Ile	Ala	Lys	His	Thr	Arg	Met	Ser	Pro	Gln	Gln	Arg	Leu	
				245					250					255		
Asp	Glu	Thr	Arg	Lys	Leu	Ile	Thr	Lys	Leu	Ser	Gln	Asn	Gln	Thr	Met	
			260					265					270			
Met	Glu	Cys	Phe	Gln	Tyr	Trp	Gly	Ile	Ser	Leu	Gly	Gln	Asp	Leu	Ala	
		275					280					285				

10029493.10601

Asn	Val	Gln	Ala	Arg	Val	Leu	Lys	Ser	Glu	Pro	Leu	Gln	Gly	Lys	Arg	290	295	300	
Gln	Tyr	Glu	Gly	Lys	Gln	Ala	Glu	Trp	Ala	Arg	Gly	Val	Lys	Glu	Cys	305	310	315	320
Gly	Ile	Tyr	Arg	Gly	Ser	Asn	Met	Thr	Asn	Trp	Ile	Val	Ile	Gly	Pro	325	330	335	
Gly	Ser	Gly	Asn	Ser	Gly	Leu	Leu	Ala	Gln	Lys	Phe	Ile	Ala	Glu	Ala	340	345	350	
Arg	Asn	Leu	Gly	Arg	Thr	Leu	Gln	Val	Gln	Leu	Gly	Glu	Pro	Met	Cys	355	360	365	
Val	Lys	Ile	Asn	Gly	Ile	Ser	Pro	Asn	Asp	Tyr	Leu	Glu	Gly	Leu	Lys	370	375	380	
Ala	Ala	Ile	Lys	Ser	Val	Asp	Gly	Glu	Glu	Ile	His	Met	Leu	Val	Val	385	390	395	400
Met	Leu	Ala	Asp	Asp	Asn	Lys	Thr	Arg	Tyr	Asp	Ser	Leu	Lys	Lys	Tyr	405	410	415	
Leu	Cys	Val	Glu	Cys	Pro	Ile	Pro	Asn	Gln	Cys	Val	Asn	Leu	Arg	Thr	420	425	430	
Leu	Ala	Gly	Lys	Ser	Lys	Asp	Gly	Gly	Glu	Asn	Lys	Asn	Leu	Gly	Ser	435	440	445	
Ile	Val	Leu	Lys	Ile	Val	Leu	Gln	Met	Ile	Cys	Lys	Thr	Gly	Gly	Ala	450	455	460	
Leu	Trp	Lys	Val	Asn	Ile	Pro	Leu	Lys	Ser	Thr	Met	Ile	Val	Gly	Tyr	465	470	475	480
Asp	Leu	Tyr	His	Asp	Ser	Thr	Leu	Lys	Gly	Lys	Thr	Val	Gly	Ala	Cys	485	490	495	
Val	Ser	Thr	Thr	Ser	Asn	Asp	Phe	Thr	Gln	Phe	Tyr	Ser	Gln	Thr	Arg	500	505	510	
Pro	His	Glu	Asn	Pro	Thr	Gln	Leu	Gly	Asn	Asn	Leu	Thr	His	Phe	Val	515	520	525	
Arg	Lys	Ser	Leu	Lys	Gln	Tyr	Tyr	Asp	Asn	Asn	Asp	Lys	Thr	Leu	Pro	530	535	540	
Ser	Arg	Leu	Ile	Leu	Tyr	Arg	Asp	Gly	Ala	Gly	Asp	Gly	Gln	Ile	Pro	545	550	555	560
Tyr	Ile	Lys	Asn	Thr	Glu	Val	Lys	Leu	Val	Arg	Asp	Ala	Cys	Asp	Ala	565	570	575	
Val	Thr	Asp	Lys	Ala	Ala	Glu	Leu	Ser	Asn	Lys	Val	Gln	Glu	Lys	Ile	580	585	590	
Lys	Leu	Ala	Phe	Ile	Ile	Val	Thr	Lys	Arg	Val	Asn	Met	Arg	Ile	Leu	595	600	605	

10029495-100304

Lys Gln Gly Ser Ser Ser Lys Ser Ala Ile Asn Pro Gln Pro Gly Thr
610 615 620
Val Val Asp Thr Thr Val Thr Arg Pro Glu Arg Met Asp Phe Tyr Leu
625 630 635 640
Val Pro Gln Phe Val Asn Gln Gly Thr Val Thr Pro Val Ser Tyr Asn
645 650 655
Ile Ile His Asp Asp Thr Gly Leu Gly Pro Asp Lys His Gln Gln Leu
660 665 670
Ala Phe Lys Leu Cys His Leu Tyr Tyr Asn Trp Gln Gly Thr Val Arg
675 680 685
Val Pro Ala Pro Cys Gln Tyr Ala His Lys Leu Ala Phe Leu Thr Ala
690 695 700
Gln Ser Leu His Asp Asp Ala Asn Gly Tyr Leu Arg Asp Lys Leu Phe
705 710 715 720
Phe Leu

<210> 6
<211> 824
<212> PRT
<213> Caenorhabditis elegans

<220>
<223> ciwi2

<400> 6
Met Ala Ser Gly Ser Gly Arg Gly Arg Gly Arg Gly Ser Gly Ser Asn
1 5 10 15
Asn Ser Gly Gly Lys Asp Gln Lys Tyr Leu Gly Thr Ile Gln Pro Asp
20 25 30
Leu Phe Ile Arg Gln Gln Gly Gln Ser Lys Thr Gly Ser Ser Gly Gln
35 40 45
Pro Gln Lys Cys Phe Ala Asn Phe Ile Pro Ile Glu Met Thr Gln Ser
50 55 60
Asp Tyr Ser Ile Tyr Gln Tyr His Val Glu Phe Glu Pro Thr Val Asp
65 70 75 80
Ser Lys Ala Asn Arg Glu Lys Met Leu Arg Asp Asn Asn Val Thr Asp
85 90 95
Glu Ile Gly His His Phe Val Phe Asp Gly Met Ile Leu Tyr Leu Lys
100 105 110
Glu Glu Trp Glu Gln Asn Gln Met Ile Glu Val Gln His Pro Ile Asp
115 120 125
Arg Ser Leu Ile Cys Ile Arg Phe Lys Gln Thr Asn Arg Phe Leu Val
130 135 140
Asp Asp Pro Gln Thr Ile Asn Ile Phe Asn Thr Ile Ile Arg Arg Ser
145 150 155 160

T0020T "5545200T

Phe Asp Ala Leu Gln Leu Thr Gln Leu Gly Arg Asn Tyr Phe Asn Trp
165 170 175

Gly Asp Ser Arg Ala Val Pro Asp Tyr Asn Met Ser Ile Leu Pro Gly
180 185 190

Tyr Glu Thr Ala Ile Arg Met Tyr Glu Glu Asn Phe Met Leu Cys Val
195 200 205

Glu Asn Arg Phe Lys Met Val Arg Glu Glu Ser Met Tyr Ile Leu Phe
210 215 220

His Lys Glu Leu Arg Ser Cys Gln Asn Asn Pro Gln Arg Val Gln Glu
225 230 235 240

Lys Met Asn Glu Met Tyr Gly Gly Thr Thr Ile Ile Thr Arg Tyr Asn
245 250 255

Asn Lys Leu His Arg Tyr Thr Arg Leu Asp Tyr Ser Ile Ser Pro Leu
260 265 270

Ser Glu Phe Val Lys Asp Gly Gln Ser Ile Thr Leu Lys Glu Tyr Phe
275 280 285

Lys Asn Gln Tyr Gly Ile Glu Ile Thr Val Asp Asp Gln Pro Ile Ile
290 295 300

Ile Ser Glu Gly Lys Pro Lys Gln Pro Gly Glu Pro Pro Gln Val Ser
305 310 315 320

Tyr Ile Val Pro Glu Leu Cys Phe Pro Thr Gly Leu Thr Asp Glu Met
325 330 335

Arg Lys Asp Phe Lys Met Met Lys Glu Ile Ala Lys His Thr Arg Met
340 345 350

Ser Pro Gln Gln Arg Leu Val Glu Ser Arg Lys Leu Ile Val Asp Leu
355 360 365

Ser Lys Asn Glu Lys Val Met Glu Cys Phe Lys Tyr Trp Gly Ile Ser
370 375 380

Leu Gly Gln Asp Leu Ala Asn Val Gln Ala Arg Val Leu Lys Ser Glu
385 390 395 400

Pro Leu Gln Gly Lys Lys Thr Tyr Glu Gly Lys Gln Ala Glu Trp Ala
405 410 415

Arg Gly Val Lys Glu Cys Gly Ile Tyr Arg Gly Ser Asn Met Thr Asn
420 425 430

Trp Ile Val Ile Gly Pro Gly Ser Gly Asn Ser Gly Leu Leu Ser Gln
435 440 445

Lys Phe Ile Glu Glu Ala Arg Arg Leu Gly Lys Ile Leu Gln Val Gln
450 455 460

Leu Gly Glu Pro Met Cys Val Pro Ile Arg Gly Ile Ser Pro Asn Asp
465 470 475 480

Tyr Leu Glu Gly Val Lys Gly Ala Ile Lys Gln Val Asp Gly Glu Asp
485 490 495

10025435-102001

10029495-100301

Ile	His	Met	Leu	Val	Val	Met	Leu	Ala	Asp	Asp	Asn	Lys	Thr	Arg	Tyr	500	505	510
Asp	Ser	Leu	Lys	Lys	Phe	Leu	Cys	Val	Glu	Cys	Pro	Ile	Pro	Asn	Gln	515	520	525
Cys	Val	Asn	Leu	Arg	Thr	Leu	Ala	Gly	Lys	Ser	Lys	Asp	Gly	Gly	Glu	530	535	540
Asn	Lys	Asn	Leu	Gly	Ser	Ile	Val	Leu	Lys	Ile	Val	Leu	Gln	Met	Ile	545	550	555
Cys	Lys	Thr	Gly	Gly	Ala	Leu	Trp	Lys	Val	Asn	Ile	Pro	Leu	Lys	Asn	565	570	575
Thr	Met	Ile	Val	Gly	Tyr	Asp	Leu	Tyr	His	Asp	Ser	Thr	Leu	Lys	Gly	580	585	590
Lys	Thr	Val	Gly	Ala	Cys	Val	Ser	Thr	Thr	Ser	Asn	Asp	Phe	Thr	Gln	595	600	605
Phe	Tyr	Ser	Gln	Thr	Arg	Pro	His	Glu	Asn	Pro	Thr	Gln	Leu	Gly	Asn	610	615	620
Asn	Leu	Thr	His	Phe	Val	Arg	Lys	Ala	Leu	Lys	Gln	Tyr	Tyr	Asp	Ser	625	630	635
Asn	Asp	Gln	Thr	Leu	Pro	Ser	Arg	Leu	Ile	Leu	Tyr	Arg	Asp	Gly	Ala	645	650	655
Gly	Asp	Gly	Gln	Ile	Pro	Tyr	Ile	Lys	Asn	Thr	Glu	Val	Lys	Leu	Val	660	665	670
Arg	Asp	Ala	Cys	Asp	Ala	Val	Thr	Asp	Lys	Ala	Ala	Glu	Leu	Ser	Asn	675	680	685
Lys	Val	Gln	Glu	Lys	Ile	Lys	Leu	Ala	Phe	Ile	Ile	Val	Thr	Lys	Arg	690	695	700
Val	Asn	Met	Arg	Ile	Leu	Lys	Gln	Gly	Ser	Ser	Leu	Asp	Asn	Ala	Ile	705	710	715
Asn	Pro	Gln	Pro	Gly	Thr	Val	Val	Asp	Thr	Thr	Val	Thr	Arg	Pro	Glu	725	730	735
Arg	Met	Asp	Phe	Tyr	Leu	Val	Pro	Gln	Phe	Val	Asn	Gln	Gly	Thr	Val	740	745	750
Thr	Pro	Val	Ser	Tyr	Asn	Ile	Ile	His	Asp	Asp	Thr	Asp	Leu	Gly	Pro	755	760	765
Asp	Lys	His	Gln	Gln	Leu	Ala	Phe	Lys	Leu	Cys	His	Leu	Tyr	Tyr	Asn	770	775	780
Trp	Gln	Gly	Thr	Val	Arg	Val	Pro	Ala	Pro	Cys	Gln	Tyr	Ala	His	Lys	785	790	795
Leu	Ala	Phe	Leu	Thr	Ala	Gln	Ser	Leu	His	Asp	Asp	Ala	Asn	Gly	Cys	805	810	815

Leu Arg Asp Lys Leu Phe Phe Leu
820

<210> 7

<211> 844

<212> PRT

<213> Drosophila

<220>

<223> piwi

<400> 7

Met Ala Asp Asp Gln Gly Arg Gly Arg Arg Arg Pro Leu Asn Glu Asp
1 5 10 15

Asp Ser Ser Thr Ser Arg Gly Ser Gly Asp Gly Pro Arg Val Lys Val
20 25 30

Phe Arg Gly Ser Ser Ser Gly Asp Pro Arg Ala Asp Pro Arg Ile Glu
35 40 45

Ala Ser Arg Glu Arg Arg Ala Leu Glu Glu Ala Pro Arg Arg Glu Gly
50 55 60

Gly Pro Thr Glu Arg Lys Pro Trp Gly Asp Gln Tyr Asp Tyr Leu Asn
65 70 75 80

Thr Arg Pro Ala Glu Leu Val Ser Lys Lys Gly Thr Asp Gly Val Pro
85 90 95

Val Met Leu Gln Thr Asn Phe Phe Arg Leu Lys Thr Lys Pro Glu Trp
100 105 110

Arg Ile Val His Tyr His Val Glu Phe Glu Pro Ser Ile Glu Asn Pro
115 120 125

Arg Val Arg Met Gly Val Leu Ser Asn His Ala Asn Leu Leu Gly Ser
130 135 140

Gly Tyr Leu Phe Asp Gly Leu Gln Leu Phe Thr Thr Arg Lys Phe Glu
145 150 155 160

Gln Glu Ile Thr Val Leu Ser Gly Lys Ser Lys Leu Asp Ile Glu Tyr
165 170 175

Lys Ile Ser Ile Lys Phe Val Gly Phe Ile Ser Cys Ala Glu Pro Arg
180 185 190

Phe Leu Gln Val Leu Asn Leu Ile Leu Arg Arg Ser Met Lys Gly Leu
195 200 205

Asn Leu Glu Leu Val Gly Arg Asn Leu Phe Asp Pro Arg Ala Lys Ile
210 215 220

Glu Ile Arg Glu Phe Lys Met Glu Leu Trp Pro Gly Tyr Glu Thr Ser
225 230 235 240

Ile Arg Gln His Glu Lys Asp Ile Leu Leu Gly Thr Glu Ile Thr His
245 250 255

Lys Val Met Arg Thr Glu Thr Ile Tyr Asp Ile Met Arg Arg Cys Ser
260 265 270

TOGETHER

His	Asn	Pro	Ala	Arg	His	Gln	Asp	Glu	Val	Arg	Val	Asn	Val	Leu	Asp
		275					280					285			
Leu	Ile	Val	Leu	Thr	Asp	Tyr	Asn	Asn	Arg	Thr	Tyr	Arg	Ile	Asn	Asp
	290					295					300				
Val	Asp	Phe	Gly	Gln	Thr	Pro	Lys	Ser	Thr	Phe	Ser	Cys	Lys	Gly	Arg
305					310					315					320
Asp	Ile	Ser	Phe	Val	Glu	Tyr	Tyr	Leu	Thr	Lys	Tyr	Asn	Ile	Arg	Ile
				325					330					335	
Arg	Asp	His	Asn	Gln	Pro	Leu	Leu	Ile	Ser	Lys	Asn	Arg	Asp	Lys	Ala
			340					345					350		
Leu	Lys	Thr	Asn	Ala	Ser	Glu	Leu	Val	Val	Leu	Ile	Pro	Glu	Leu	Cys
		355					360					365			
Arg	Val	Thr	Gly	Leu	Asn	Ala	Glu	Met	Arg	Ser	Asn	Phe	Gln	Leu	Met
	370					375					380				
Arg	Ala	Met	Ser	Ser	Tyr	Thr	Arg	Met	Asn	Pro	Lys	Gln	Arg	Thr	Asp
385					390					395					400
Arg	Leu	Arg	Ala	Phe	Asn	His	Arg	Leu	Gln	Asn	Thr	Pro	Glu	Ser	Val
			405						410					415	
Lys	Val	Leu	Arg	Asp	Trp	Asn	Met	Glu	Leu	Asp	Lys	Asn	Val	Thr	Glu
		420						425					430		
Val	Gln	Gly	Arg	Ile	Ile	Gly	Gln	Gln	Asn	Ile	Val	Phe	His	Asn	Gly
	435						440					445			
Lys	Val	Pro	Ala	Gly	Glu	Asn	Ala	Asp	Trp	Gln	Arg	His	Phe	Arg	Asp
	450					455					460				
Gln	Arg	Met	Leu	Thr	Thr	Pro	Ser	Asp	Gly	Leu	Asp	Arg	Trp	Ala	Val
465					470					475					480
Ile	Ala	Pro	Gln	Arg	Asn	Ser	His	Glu	Leu	Arg	Thr	Leu	Leu	Asp	Ser
			485						490					495	
Leu	Tyr	Arg	Ala	Ala	Ser	Gly	Met	Gly	Leu	Arg	Ile	Arg	Ser	Pro	Gln
			500					505					510		
Glu	Phe	Ile	Ile	Tyr	Asp	Asp	Arg	Thr	Gly	Thr	Tyr	Val	Arg	Ala	Met
	515						520					525			
Asp	Asp	Cys	Val	Arg	Ser	Asp	Pro	Lys	Leu	Ile	Leu	Cys	Leu	Val	Pro
	530					535					540				
Asn	Asp	Asn	Ala	Glu	Arg	Tyr	Ser	Ser	Ile	Lys	Lys	Arg	Gly	Tyr	Val
545					550					555					560
Asp	Arg	Ala	Val	Pro	Thr	Gln	Val	Val	Thr	Leu	Lys	Thr	Thr	Lys	Lys
			565						570					575	
Pro	Tyr	Ser	Leu	Met	Ser	Ile	Ala	Thr	Lys	Ile	Ala	Ile	Gln	Leu	Asn
			580					585					590		
Cys	Lys	Leu	Gly	Tyr	Thr	Pro	Trp	Met	Ile	Glu	Leu	Pro	Leu	Ser	Gly
		595					600					605			

Leu	Met	Thr	Ile	Gly	Phe	Asp	Ile	Ala	Lys	Ser	Thr	Arg	Asp	Arg	Lys
610						615					620				
Arg	Ala	Tyr	Gly	Ala	Leu	Ile	Ala	Ser	Met	Asp	Leu	Gln	Gln	Asn	Ser
625					630					635					640
Thr	Tyr	Phe	Ser	Thr	Val	Thr	Glu	Cys	Ser	Ala	Phe	Asp	Val	Leu	Ala
				645					650					655	
Asn	Thr	Leu	Trp	Pro	Met	Ile	Ala	Lys	Ala	Leu	Arg	Gln	Tyr	Gln	His
			660					665					670		
Glu	His	Arg	Lys	Leu	Pro	Ser	Arg	Ile	Val	Phe	Tyr	Arg	Asp	Gly	Val
		675					680					685			
Ser	Ser	Gly	Ser	Leu	Lys	Gln	Leu	Phe	Glu	Phe	Glu	Val	Lys	Asp	Ile
	690					695					700				
Ile	Glu	Lys	Leu	Lys	Thr	Glu	Tyr	Ala	Arg	Val	Gln	Leu	Ser	Pro	Pro
705					710					715					720
Gln	Leu	Ala	Tyr	Ile	Val	Val	Thr	Arg	Ser	Met	Asn	Thr	Arg	Phe	Phe
				725					730					735	
Leu	Asn	Gly	Gln	Asn	Pro	Pro	Pro	Gly	Thr	Ile	Val	Asp	Asp	Val	Ile
			740					745					750		
Thr	Leu	Pro	Glu	Arg	Tyr	Asp	Phe	Tyr	Leu	Val	Ser	Gln	Gln	Val	Arg
		755					760					765			
Gln	Gly	Thr	Val	Ser	Pro	Thr	Ser	Tyr	Asn	Val	Leu	Tyr	Ser	Ser	Met
	770					775					780				
Gly	Leu	Ser	Pro	Glu	Lys	Met	Gln	Lys	Leu	Thr	Tyr	Lys	Met	Cys	His
785					790					795					800
Leu	Tyr	Tyr	Asn	Trp	Ser	Gly	Thr	Thr	Arg	Val	Pro	Ala	Val	Cys	Gln
			805						810					815	
Tyr	Ala	Lys	Lys	Leu	Ala	Thr	Leu	Val	Gly	Thr	Asn	Leu	His	Ser	Ile
			820					825					830		
Pro	Gln	Asn	Ala	Leu	Glu	Lys	Lys	Phe	Tyr	Tyr	Leu				
		835					840								

<210> 8

<211> 2009

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (73) .. (1569)

<400> 8
gcggccgctg aattctaggt ggattactac aagcagcagt atgatattac tgtatcggac 60
ctgaatcagc cc atg ctt gtt agt ctg tta aag aag aag aga aat gac aac 111
Met Leu Val Ser Leu Leu Lys Lys Lys Arg Asn Asp Asn
1 5 10
agt gag cct cag ctg gcc cac ctg ata cct gag ctg tgc ttt cta aca 159
Ser Glu Pro Gln Leu Ala His Leu Ile Pro Glu Leu Cys Phe Leu Thr
15 20 25
ggg ctg act gac cag gca aca tct gat ttc cag ctg atg aag gct gtg 207
Gly Leu Thr Asp Gln Ala Thr Ser Asp Phe Gln Leu Met Lys Ala Val
30 35 40 45
gct gaa aag aca cgt ctg agt cct tca ggc cgg cag cag cgc ctg gcc 255
Ala Glu Lys Thr Arg Leu Ser Pro Ser Gly Arg Gln Gln Arg Leu Ala
50 55 60
agg ctt gtg gac aac atc cag agg aat acc aat gct cgc ttt gaa cta 303
Arg Leu Val Asp Asn Ile Gln Arg Asn Thr Asn Ala Arg Phe Glu Leu
65 70 75
gag acc tgg gga ctg cat ttt gga agc cag ata tct ctg act ggc cgg 351
Glu Thr Trp Gly Leu His Phe Gly Ser Gln Ile Ser Leu Thr Gly Arg
80 85 90
att gtg cct tca gaa aaa ata tta atg caa gac cac ata tgt caa cct 399
Ile Val Pro Ser Glu Lys Ile Leu Met Gln Asp His Ile Cys Gln Pro
95 100 105
gtg tct gct gct gac tgg tcc aag gat att cga act tgc aag att tta 447
Val Ser Ala Ala Asp Trp Ser Lys Asp Ile Arg Thr Cys Lys Ile Leu
110 115 120 125
aat gca cag tct ttg aat acc tgg ttg att tta tgt agc gac aga act 495
Asn Ala Gln Ser Leu Asn Thr Trp Leu Ile Leu Cys Ser Asp Arg Thr
130 135 140
gaa tat gtt gcc gag agc ttt ctg aac tgc ttg aga aga gtt gca ggt 543
Glu Tyr Val Ala Glu Ser Phe Leu Asn Cys Leu Arg Arg Val Ala Gly
145 150 155
tcc atg gga ttt aat gtg gac tac ccc aaa atc ata aaa gta caa gaa 591
Ser Met Gly Phe Asn Val Asp Tyr Pro Lys Ile Ile Lys Val Gln Glu
160 165 170
aat cca gct gca ttt gtt aga gct ata cag caa tat gtt gat cct gat 639
Asn Pro Ala Ala Phe Val Arg Ala Ile Gln Gln Tyr Val Asp Pro Asp
175 180 185
gtt cag ctg gta atg tgc att ctg cct tct aat cag aag acc tat tat 687
Val Gln Leu Val Met Cys Ile Leu Pro Ser Asn Gln Lys Thr Tyr Tyr
190 195 200 205
gat tcc att aaa aaa tat ttg agc tca gac tgc cca gtc cca agc caa 735
Asp Ser Ile Lys Lys Tyr Leu Ser Ser Asp Cys Pro Val Pro Ser Gln
210 215 220

00245-0001-0001

tgt gtg ctt gct cgg acc ttg aat aaa cag ggc atg atg atg agt atc Cys Val Leu Ala Arg Thr Leu Asn Lys Gln Gly Met Met Met Ser Ile 225 230 235	783
gcc acc aag atc gct atg cag atg act tgc aag ctc gga ggc gag ctg Ala Thr Lys Ile Ala Met Gln Met Thr Cys Lys Leu Gly Gly Glu Leu 240 245 250	831
tgg gct gtg gaa ata cct tta aag tcc ctg atg gtg gtc ggt att gat Trp Ala Val Glu Ile Pro Leu Lys Ser Leu Met Val Val Gly Ile Asp 255 260 265	879
gtc tgt aaa gat gca ctc agc aag gac gtg atg gtt gtt gga tgc gtg Val Cys Lys Asp Ala Leu Ser Lys Asp Val Met Val Val Gly Cys Val 270 275 280 285	927
gcc agt gtt aac ccc aga atc acc agg tgg ttt tcc cgc tgt atc ctt Ala Ser Val Asn Pro Arg Ile Thr Arg Trp Phe Ser Arg Cys Ile Leu 290 295 300	975
cag aga aca atg act gat gtt gca gat tgc ttg aaa gtt ttc atg act Gln Arg Thr Met Thr Asp Val Ala Asp Cys Leu Lys Val Phe Met Thr 305 310 315	1023
gga gca ctc aac aaa tgg tac aag tac aat cat gat ttg cca gca cgg Gly Ala Leu Asn Lys Trp Tyr Lys Tyr Asn His Asp Leu Pro Ala Arg 320 325 330	1071
ata att gtg tac cgt gct ggt gta ggg gat ggt cag ctg aaa aca ctt Ile Ile Val Tyr Arg Ala Gly Val Gly Asp Gly Gln Leu Lys Thr Leu 335 340 345	1119
att gaa tat gaa gtc cca cag ctg ctg agc agt gtg gca gaa tcc agc Ile Glu Tyr Glu Val Pro Gln Leu Leu Ser Ser Val Ala Glu Ser Ser 350 355 360 365	1167
tca aat acc agc tca aga ctg tgc gtg att gtg gtc agg aag aag tgc Ser Asn Thr Ser Ser Arg Leu Ser Val Ile Val Val Arg Lys Lys Cys 370 375 380	1215
atg cca cga ttc ttt acc gaa atg aac cgc act gta cag aac ccc cca Met Pro Arg Phe Phe Thr Glu Met Asn Arg Thr Val Gln Asn Pro Pro 385 390 395	1263
ctt ggc act gtt gtg gat tca gaa gca aca cgt aac gaa tgg tat gac Leu Gly Thr Val Val Asp Ser Glu Ala Thr Arg Asn Glu Trp Tyr Asp 400 405 410	1311
ttt tat ctg atc agc cag gtg gcc tgc cgg gga act gtt agt cct acc Phe Tyr Leu Ile Ser Gln Val Ala Cys Arg Gly Thr Val Ser Pro Thr 415 420 425	1359
tac tat aat gtc atc tat gat gac aac ggc ttg aag ccc gac cat atg Tyr Tyr Asn Val Ile Tyr Asp Asp Asn Gly Leu Lys Pro Asp His Met 430 435 440 445	1407
cag aga ctt aca ttc aaa ttg tgc cac ctg tac tac aac tgg ccg ggc Gln Arg Leu Thr Phe Lys Leu Cys His Leu Tyr Tyr Asn Trp Pro Gly 450 455 460	1455
ata gtc agt gtc cca gca cca tgt cag tat gct cac aag ctg acc ttt Ile Val Ser Val Pro Ala Pro Cys Gln Tyr Ala His Lys Leu Thr Phe 465 470 475	1503

Ser Glu Lys Ile Leu Met Gln Asp His Ile Cys Gln Pro Val Ser Ala
100 105 110

Ala	Asp	Trp	Ser	Lys	Asp	Ile	Arg	Thr	Cys	Lys	Ile	Leu	Asn	Ala	Gln		
	115						120					125					
Ser	Leu	Asn	Thr	Trp	Leu	Ile	Leu	Cys	Ser	Asp	Arg	Thr	Glu	Tyr	Val		
	130					135					140						
Ala	Glu	Ser	Phe	Leu	Asn	Cys	Leu	Arg	Arg	Val	Ala	Gly	Ser	Met	Gly		
145					150					155					160		
Phe	Asn	Val	Asp	Tyr	Pro	Lys	Ile	Ile	Lys	Val	Gln	Glu	Asn	Pro	Ala		
			165						170						175		
Ala	Phe	Val	Arg	Ala	Ile	Gln	Gln	Tyr	Val	Asp	Pro	Asp	Val	Gln	Leu		
			180					185						190			
Val	Met	Cys	Ile	Leu	Pro	Ser	Asn	Gln	Lys	Thr	Tyr	Tyr	Asp	Ser	Ile		
		195					200						205				
Lys	Lys	Tyr	Leu	Ser	Ser	Asp	Cys	Pro	Val	Pro	Ser	Gln	Cys	Val	Leu		
	210					215						220					
Ala	Arg	Thr	Leu	Asn	Lys	Gln	Gly	Met	Met	Met	Ser	Ile	Ala	Thr	Lys		
225					230					235					240		
Ile	Ala	Met	Gln	Met	Thr	Cys	Lys	Leu	Gly	Gly	Glu	Leu	Trp	Ala	Val		
				245					250					255			
Glu	Ile	Pro	Leu	Lys	Ser	Leu	Met	Val	Val	Gly	Ile	Asp	Val	Cys	Lys		
			260					265						270			
Asp	Ala	Leu	Ser	Lys	Asp	Val	Met	Val	Val	Gly	Cys	Val	Ala	Ser	Val		
		275					280					285					
Asn	Pro	Arg	Ile	Thr	Arg	Trp	Phe	Ser	Arg	Cys	Ile	Leu	Gln	Arg	Thr		
	290					295					300						
Met	Thr	Asp	Val	Ala	Asp	Cys	Leu	Lys	Val	Phe	Met	Thr	Gly	Ala	Leu		
305					310					315					320		
Asn	Lys	Trp	Tyr	Lys	Tyr	Asn	His	Asp	Leu	Pro	Ala	Arg	Ile	Ile	Val		
				325					330					335			
Tyr	Arg	Ala	Gly	Val	Gly	Asp	Gly	Gln	Leu	Lys	Thr	Leu	Ile	Glu	Tyr		
		340						345					350				
Glu	Val	Pro	Gln	Leu	Leu	Ser	Ser	Val	Ala	Glu	Ser	Ser	Ser	Asn	Thr		
		355					360						365				

- 20 -

Ser Ser Arg Leu Ser Val Ile Val Val Arg Lys Lys Cys Met Pro Arg
370 375 380

Phe Phe Thr Glu Met Asn Arg Thr Val Gln Asn Pro Pro Leu Gly Thr
385 390 395 400

Val Val Asp Ser Glu Ala Thr Arg Asn Glu Trp Tyr Asp Phe Tyr Leu
405 410 415

Ile Ser Gln Val Ala Cys Arg Gly Thr Val Ser Pro Thr Tyr Tyr Asn
420 425 430

Val Ile Tyr Asp Asp Asn Gly Leu Lys Pro Asp His Met Gln Arg Leu
435 440 445

Thr Phe Lys Leu Cys His Leu Tyr Tyr Asn Trp Pro Gly Ile Val Ser
450 455 460

Val Pro Ala Pro Cys Gln Tyr Ala His Lys Leu Thr Phe Leu Gly Ala
465 470 475 480

Gln Ser Ile His Lys Glu Pro Ser Leu Glu Leu Ala Asn His Leu Phe
485 490 495

Tyr Leu

<210> 10

<211> 24

<212> DNA

<213> synthetic - pSPORT VP1

<400> 10
aggcaccocca ggctttacac ttta

24

<210> 11

<211> 21

<212> DNA

<213> synthetic - pSPORT VP2

<400> 11
ttccccggggtc gacgatttcg t

21

protein sequence

<210> 12

<211> 27

<212> DNA

<213> synthetic - cDNA VP1

<400> 12

ccatcctaatacgcactcactatagggc

27

<210> 13

<211> 23

<212> DNA

<213> synthetic - Marathon cDNA VP2

<400> 13

actcactatagggctcgagcggc

23

TE0920T "5546200T"